

# SCORE Search Results Details for Application 10565283 and Search Result 20070524\_163504\_us-10-565-283- 1\_copy\_474\_494.sl.rnpbn.

|                            |                                      |                              |                       |                             |
|----------------------------|--------------------------------------|------------------------------|-----------------------|-----------------------------|
| <a href="#">Score Home</a> | <a href="#">Retrieve Application</a> | <a href="#">SCORE System</a> | <a href="#">SCORE</a> | <a href="#">Comments /</a>  |
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2007, 22:00:12 ; Search time 573 Seconds  
(without alignments)  
349.228 Million cell updates/sec

Title: US-10-565-283-1\_COPY\_474\_494  
Perfect score: 21  
Sequence: 1 gaacttggaagaggggagcca 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: , 15567911 seqs, 4762600769 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 10  
Maximum DB seq length: 22

Post-processing: Minimum Score over Length 100%  
Listing first 500 summaries

Database : Published\_Applications\_NA\_New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq1:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq2:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq3:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq4:\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq5:\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq6:\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq1:\*

```
15: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
16: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
17: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
18: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq5:*
19: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq6:*
20: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq7:*
21: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq8:*
22: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result | Score | %      | Query |        |    |    |  |             |
|--------|-------|--------|-------|--------|----|----|--|-------------|
| No.    | Score | Length | Match | Length | DB | ID |  | Description |

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No matches found

Search completed: May 27, 2007, 23:23:15  
Job time : 572.775 secs

|                                 |
|---------------------------------|
| SCORE 2.0 BuildDate: 12/05/2005 |
|---------------------------------|

## SCORE Search Results Details for Application 10565283 and Search Result 20070524\_163504\_ 10-565-283-1\_copy\_187\_205.sl.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on: May 27, 2007, 22:00:12 ; Search time 518 Seconds  
(without alignments)  
349.228 Million cell updates/sec

Title: US-10-565-283-1\_COPY\_187\_205  
Perfect score: 19  
Sequence: 1 cgggatgtttccagtgcaca 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 15567911 seqs, 4762600769 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 10  
Maximum DB seq length: 22

Post-processing: Minimum Score over Length 100%  
Listing first 500 summaries

Database : Published\_Applications\_NA\_New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq1:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq2:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq3:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq4:\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq5:\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq6:\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq1:\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq2:\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq3:\*
- 17: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq4:\*

18: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq5:\*  
 19: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq6:\*  
 20: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq7:\*  
 21: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq8:\*  
 22: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result | Score | %     |       |        |    |                 |             |  |
|--------|-------|-------|-------|--------|----|-----------------|-------------|--|
| No.    | over  | Query | Match | Length | DB | ID              | Description |  |
| 1      | 19    | 100.0 | 100.0 | 19     | 6  | US-10-565-283-4 | Sequence 4  |  |
| c 2    | 19    | 100.0 | 100.0 | 19     | 6  | US-10-565-283-5 | Sequence 5  |  |

## ALIGNMENTS

## RESULT 1

US-10-565-283-4

; Sequence 4, Application US/10565283

; Publication No. US20070049540A1

; GENERAL INFORMATION:

; APPLICANT: Japan Science and Technology Agency

; TITLE OF INVENTION: Oligonucleotide Inhibiting The Expression of StAR-Binding Prote

; TITLE OF INVENTION: Gene and Method Therefor

; FILE REFERENCE: FS04-410PCT

; CURRENT APPLICATION NUMBER: US/10/565,283

; CURRENT FILING DATE: 2006-01-20

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: siRNA

US-10-565-283-4

Query Match 100.0%; Score 19; DB 6; Length 19;

Score over Length 100.0%;

Best Local Similarity 73.7%; Pred. No. 9.2;

Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGATGTTTCCAGTGACA 19

|||||:|:::||||:||||

Db 1 CGGGAUGUUUCCAGUGACA 19

## RESULT 2

US-10-565-283-5/c

; Sequence 5, Application US/10565283

; Publication No. US20070049540A1

; GENERAL INFORMATION:

; APPLICANT: Japan Science and Technology Agency

; TITLE OF INVENTION: Oligonucleotide Inhibiting The Expression of StAR-Binding Prote

; TITLE OF INVENTION: Gene and Method Therefor

# SCORE Search Results Details for Application 10565283 and Search Result 20070524\_163504\_us-1...

; FILE REFERENCE: FS04-410PCT  
; CURRENT APPLICATION NUMBER: US/10/565,283  
; CURRENT FILING DATE: 2006-01-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: siRNA  
US-10-565-283-5

Query Match 100.0%; Score 19; DB 6; Length 19;  
Score over Length 100.0%;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGATGTTTCCAGTGACA 19  
|||  
Db 19 CGGGATGTTTCCAGTGACA 1

Search completed: May 27, 2007, 23:23:15  
Job time : 518.225 secs

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SCORE 2.0 BuildDate: 12/05/2005

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